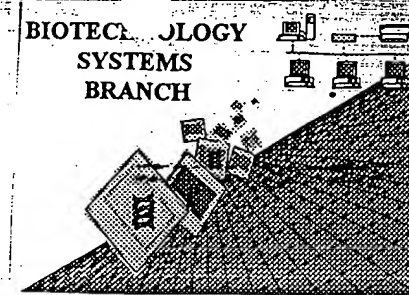


*C. Winkler*

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/254,966

Source: 1648

Date Processed by STIC: 01-25-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/254,966

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966

DATE: 01/25/2001  
TIME: 23:33:06

INPUT SET: S35457.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT:

~~(A) NAME: Bayer Aktiengesellschaft~~

. Delete

(ii) TITLE OF INVENTION: Immunogenic Peptides of Foot-and-Mouth Disease Viruses

(iii) NUMBER OF SEQUENCES: 48

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Bayer Corporation

(B) STREET: 100 Bayer Road

(C) CITY: Pittsburgh

(D) STATE: Pennsylvania

(E) ZIP CODE: 15205-9741

(F) COUNTRY: U.S.A.

(v) COMPUTER-READABLE FORM:

(A) MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS/Windows 95

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

~~(A) CURRENT APPLICATION NUMBER: 09/254,966~~

~~(B) CURRENT APPLICATION FILING DATE: March 16, 1999~~

~~(C) PRIOR APPLICATION NUMBER: PCT/EP97/04866~~

~~(D) PRIOR APPLICATION FILING DATE: September 8, 1997~~

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP97/04866

(B) FILING DATE: 8-SEPT-1997

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single-stranded

(D) TOPOLOGY: linear

Does Not Comply  
Corrected Diskette Needed

PP. 1-21

Delete

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:06

INPUT SET: S35457.raw

*molecule Type: peptide*

--> 40 (ii) ~~TYPE OF MOLECULE: peptide~~  
41  
42 (iii) HYPOTHETICAL: NO  
43  
44 (iv) ANTI-SENSE: YES  
45  
46 (v) FRAGMENT TYPE: internal fragment  
47  
48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
49  
50 Glu Arg Val His Val Met Arg Lys Thr Lys Leu Ala Pro Thr Val  
51 1        8    5        10        10    15        15  
52

This error is global.  
Please check and correct  
each of the 48 sequences.

53 (2) INFORMATION FOR SEQ ID NO: 2:  
54  
55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 15 amino acids  
57 (B) TYPE: amino acid  
58 (C) STRANDEDNESS: single-stranded  
59 (D) TOPOLOGY: linear  
60 *molecule Type: Peptide*  
--> 61 (ii) ~~TYPE OF MOLECULE: peptide~~  
62  
63 (iii) HYPOTHETICAL: NO  
64  
65 (iv) ANTI-SENSE: YES  
66  
67 (v) FRAGMENT TYPE: internal fragment  
68  
69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
70  
71 Met Arg Lys Thr Lys Leu Ala Pro Thr Val Ala His Gly Val Phe  
72 1        5    5        10        10    15        15  
73

Misaligned amino  
acid numbering. Use "spaces"  
instead of "tabs". See  
#4 on Error Summary  
Sheet. This error  
is also  
global. Please  
check and  
correct each  
sequence.

74 (2) INFORMATION FOR SEQ ID NO: 3:  
75  
76 (i) SEQUENCE CHARACTERISTICS:  
77 (A) LENGTH: 15 amino acids  
78 (B) TYPE: amino acid  
79 (C) STRANDEDNESS: single-stranded  
80 (D) TOPOLOGY: linear  
81 *molecule Type: Peptide*  
--> 82 (ii) ~~TYPE OF MOLECULE: peptide~~  
83  
84 (iii) HYPOTHETICAL: NO  
85  
86 (iv) ANTI-SENSE: YES  
87  
88 (v) FRAGMENT TYPE: internal fragment  
89  
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

The types of errors shown exist throughout the Sequence Listing. Please check  
subsequent sequences for similar errors.

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:07

INPUT SET: S35457.raw

91  
92 Leu Ala Pro Thr Val Ala His Gly Val Phe Asn Pro Glu Phe Gly  
93 1 5 10 15  
94

Error #4 refer to p.2

---

95 (2) INFORMATION FOR SEQ ID NO: 4:

96

97 (i) SEQUENCE CHARACTERISTICS:

98 (A) LENGTH: 15 amino acids

99 (B) TYPE: amino acid

100 (C) STRANDEDNESS: single-stranded

101 (D) TOPOLOGY: linear

102

--> 103 (ii) ~~TYPE OF MOLECULE: peptide~~

104

105 (iii) HYPOTHETICAL: NO

106

107 (iv) ANTI-SENSE: YES

108

109 (v) FRAGMENT TYPE: internal fragment

110

111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

112

113 Arg Cys Ala Ala Asp Tyr Ala Ser Arg Leu His Ser Val Leu Gly

114 1 5 10 15

115

Error #4

---

116 (2) INFORMATION FOR SEQ ID NO: 5:

117

118 (i) SEQUENCE CHARACTERISTICS:

119 (A) LENGTH: 15 amino acids

120 (B) TYPE: amino acid

121 (C) STRANDEDNESS: single-stranded

122 (D) TOPOLOGY: linear

123

--> 124 (ii) ~~TYPE OF MOLECULE: peptide~~

125

126 (iii) HYPOTHETICAL: NO

127

128 (iv) ANTI-SENSE: YES

129

130 (v) FRAGMENT TYPE: internal fragment

131

132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

133

134 Asn Gly Thr Val Gly Pro Glu Val Glu Ala Ala Leu Lys Leu Met

135 1 5 10 15

136

Error #4

---

137 (2) INFORMATION FOR SEQ ID NO: 6:

138

139 (i) SEQUENCE CHARACTERISTICS:

140 (A) LENGTH: 15 amino acids

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:07

INPUT SET: S35457.raw

141 (B) TYPE: amino acid  
142 (C) STRANDEDNESS: single-stranded  
143 (D) TOPOLOGY: linear  
144  
--> 145 ~~(ii) TYPE OF MOLECULE: peptide~~  
146  
147 (iii) HYPOTHETICAL: NO  
148  
149 (iv) ANTI-SENSE: YES  
150  
151 (v) FRAGMENT TYPE: internal fragment  
152  
153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
154  
155 Glu Lys Arg Glu Tyr Lys Phe Val Cys Gln Thr Phe Leu Lys Asp  
156 1 5 10 15  
157

Error #4

---

158 (2) INFORMATION FOR SEQ ID NO: 7:  
159  
160 (i) SEQUENCE CHARACTERISTICS:  
161 (A) LENGTH: 15 amino acids  
162 (B) TYPE: amino acid  
163 (C) STRANDEDNESS: single-stranded  
164 (D) TOPOLOGY: linear  
165  
--> 166 ~~(ii) TYPE OF MOLECULE: peptide~~  
167  
168 (iii) HYPOTHETICAL: NO  
169  
170 (iv) ANTI-SENSE: YES  
171  
172 (v) FRAGMENT TYPE: internal fragment  
173  
174 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
175  
176 Ala Gln Met His Ser Asn Asn Gly Pro Gln Ile Gly Ser Ala Val  
177 1 5 10 15  
178

Error #4

---

179 (2) INFORMATION FOR SEQ ID NO: 8:  
180  
181 (i) SEQUENCE CHARACTERISTICS:  
182 (A) LENGTH: 15 amino acids  
183 (B) TYPE: amino acid  
184 (C) STRANDEDNESS: single-stranded  
185 (D) TOPOLOGY: linear  
186  
--> 187 ~~(ii) TYPE OF MOLECULE: peptide~~  
188  
189 (iii) HYPOTHETICAL: NO  
190  
191 (iv) ANTI-SENSE: YES

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:07

INPUT SET: S35457.raw

192  
193 (v) FRAGMENT TYPE: internal fragment  
194  
195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
196  
197 Ile Gly Ser Ala Val Gly Cys Asn Pro Asp Val Asp Trp Gln Arg  
198 1 5 10 15  
199

Error #4

200 (2) INFORMATION FOR SEQ ID NO: 9:  
201  
202 (i) SEQUENCE CHARACTERISTICS:  
203 (A) LENGTH: 15 amino acids  
204 (B) TYPE: amino acid  
205 (C) STRANDEDNESS: single-stranded  
206 (D) TOPOLOGY: linear  
207  
--> 208 ~~(ii) TYPE OF MOLECULE: peptide~~  
209  
210 (iii) HYPOTHETICAL: NO  
211  
212 (iv) ANTI-SENSE: YES  
213  
214 (v) FRAGMENT TYPE: internal fragment  
215  
216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
217  
218 Val Trp Asp Val Asp Tyr Ser Ala Phe Asp Ala Asn His Cys Ser  
219 1 5 10 15  
220

Error #4

221 (2) INFORMATION FOR SEQ ID NO: 10:  
222  
223 (i) SEQUENCE CHARACTERISTICS:  
224 (A) LENGTH: 15 amino acids  
225 (B) TYPE: amino acid  
226 (C) STRANDEDNESS: single-stranded  
227 (D) TOPOLOGY: linear  
228  
--> 229 ~~(ii) TYPE OF MOLECULE: peptide~~  
230  
231 (iii) HYPOTHETICAL: NO  
232  
233 (iv) ANTI-SENSE: YES  
234  
235 (v) FRAGMENT TYPE: internal fragment  
236  
237 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
238  
239 Glu-Asn Lys Arg Ile Thr Val Gly Gly Gly-Met Pro Ser Gly Cys  
240 1 5 10 15  
241

242 (2) INFORMATION FOR SEQ ID NO: 11:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:08

INPUT SET: S35457.raw

243  
244 (i) SEQUENCE CHARACTERISTICS:  
245 (A) LENGTH: 15 amino acids  
246 (B) TYPE: amino acid  
247 (C) STRANDEDNESS: single-stranded  
248 (D) TOPOLOGY: linear  
249  
--> 250 (ii) ~~TYPE OF MOLECULE: peptide~~  
251  
252 (iii) HYPOTHETICAL: NO  
253  
254 (iv) ANTI-SENSE: YES  
255  
256 (v) FRAGMENT TYPE: internal fragment  
257  
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
259  
260 His Phe Lys Ser Leu Gly Gln Thr Ile Thr Pro Ala Asp Lys Ser  
261 1 5 10 15  
262

---

263 (2) INFORMATION FOR SEQ ID NO: 12:  
264  
265 (i) SEQUENCE CHARACTERISTICS:  
266 (A) LENGTH: 15 amino acids  
267 (B) TYPE: amino acid  
268 (C) STRANDEDNESS: single-stranded  
269 (D) TOPOLOGY: linear  
270  
--> 271 (ii) ~~TYPE OF MOLECULE: peptide~~  
272  
273 (iii) HYPOTHETICAL: NO  
274  
275 (iv) ANTI-SENSE: YES  
276  
277 (v) FRAGMENT TYPE: internal fragment  
278  
279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
280  
281 Leu Lys Ala Arg Asp Ile Asn Asp Ile Phe Ala Ile Leu Lys Asn  
282 1 5 10 15  
283

---

284 (2) INFORMATION FOR SEQ ID NO: 13:  
285  
286 (i) SEQUENCE CHARACTERISTICS:  
287 (A) LENGTH: 15 amino acids  
288 (B) TYPE: amino acid  
289 (C) STRANDEDNESS: single-stranded  
290 (D) TOPOLOGY: linear  
291  
--> 292 (ii) ~~TYPE OF MOLECULE: peptide~~  
293



RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:08

INPUT SET: S35457.raw

294 (iii) HYPOTHETICAL: NO  
295  
296 (iv) ANTI-SENSE: YES  
297  
298 (v) FRAGMENT TYPE: internal fragment  
299  
300 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
301  
302 Ser Glu Glu Lys Phe Val Thr Met Thr Asp Leu Val Pro Gly Ile  
303 1 5 10 15  
304

---

305 (2) INFORMATION FOR SEQ ID NO: 14:  
306  
307 (i) SEQUENCE CHARACTERISTICS:  
308 (A) LENGTH: 15 amino acids  
309 (B) TYPE: amino acid  
310 (C) STRANDEDNESS: single-stranded  
311 (D) TOPOLOGY: linear  
312  
--> 313 ~~(ii) TYPE OF MOLECULE: peptide~~  
314  
315 (iii) HYPOTHETICAL: NO  
316  
317 (iv) ANTI-SENSE: YES  
318  
319 (v) FRAGMENT TYPE: internal fragment  
320  
321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
322  
323 Val Thr Met Thr Asp Leu Val Pro Gly Ile Leu Glu Lys Gln Arg  
324 1 5 10 15  
325

---

326 (2) INFORMATION FOR SEQ ID NO: 15:  
327  
328 (i) SEQUENCE CHARACTERISTICS:  
329 (A) LENGTH: 15 amino acids  
330 (B) TYPE: amino acid  
331 (C) STRANDEDNESS: single-stranded  
332 (D) TOPOLOGY: linear  
333  
--> 334 ~~(ii) TYPE OF MOLECULE: peptide~~  
335  
336 (iii) HYPOTHETICAL: NO  
337  
338 (iv) ANTI-SENSE: YES  
339  
340 (v) FRAGMENT TYPE: internal fragment  
341  
342 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
343  
344 Thr Gly Phe Ile Pro Pro Met Ala Ser Leu Glu Asp Lys Gly Lys

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:08

INPUT SET: S35457.raw

345 1 5 10 15  
346

---

347 (2) INFORMATION FOR SEQ ID NO: 16:

348

349 (i) SEQUENCE CHARACTERISTICS:

350 (A) LENGTH: 15 amino acids

351 (B) TYPE: amino acid

352 (C) STRANDEDNESS: single-stranded

353 (D) TOPOLOGY: linear

354

--> 355 ~~(ii) TYPE OF MOLECULE: peptide~~

356

357 (iii) HYPOTHETICAL: NO

358

359 (iv) ANTI-SENSE: YES

360

361 (v) FRAGMENT TYPE: internal fragment

362

363 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

364

365 Pro Asn Thr Ser Gly Leu Glu Thr Arg Val Val Gln Ala Glu Arg

366 1 5 10 15

367

---

368 (2) INFORMATION FOR SEQ ID NO: 17:

369

370 (i) SEQUENCE CHARACTERISTICS:

371 (A) LENGTH: 15 amino acids

372 (B) TYPE: amino acid

373 (C) STRANDEDNESS: single-stranded

374 (D) TOPOLOGY: linear

375

--> 376 ~~(ii) TYPE OF MOLECULE: peptide~~

377

378 (iii) HYPOTHETICAL: NO

379

380 (iv) ANTI-SENSE: YES

381

382 (v) FRAGMENT TYPE: internal fragment

383

384 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

385

386 Glu Leu Tyr Gln Leu Thr Leu Phe Pro His Gln Phe Ile Asn Pro

387 1 5 10 15

388

---

389 (2) INFORMATION FOR SEQ ID NO: 18:

390

391 (i) SEQUENCE CHARACTERISTICS:

392 (A) LENGTH: 15 amino acids

393 (B) TYPE: amino acid

394 (C) STRANDEDNESS: single-stranded

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:09

INPUT SET: S35457.raw

395 (D) TOPOLOGY: linear  
396  
--> 397 (ii) ~~TYPE OF MOLECULE: peptide~~  
398  
399 (iii) HYPOTHETICAL: NO  
400  
401 (iv) ANTI-SENSE: YES  
402  
403 (v) FRAGMENT TYPE: internal fragment  
404  
405 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
406  
407 Val Met Val Val Ala Pro Leu Thr Val Asn Thr Glu Gly Ala Pro  
408 1 5 10 15  
409

---

410 (2) INFORMATION FOR SEQ ID NO: 19:  
411  
412 (i) SEQUENCE CHARACTERISTICS:  
413 (A) LENGTH: 15 amino acids  
414 (B) TYPE: amino acid  
415 (C) STRANDEDNESS: single-stranded  
416 (D) TOPOLOGY: linear  
417  
--> 418 (ii) ~~TYPE OF MOLECULE: peptide~~  
419  
420 (iii) HYPOTHETICAL: NO  
421  
422 (iv) ANTI-SENSE: YES  
423  
424 (v) FRAGMENT TYPE: internal fragment  
425  
426 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
427  
428 Leu Ala Gly Leu Ala Gln Tyr Tyr Thr Gln Tyr Ser Gly Thr Ile  
429 1 5 10 15  
430  
431

---

432 (2) INFORMATION FOR SEQ ID NO: 20:  
433  
434 (i) SEQUENCE CHARACTERISTICS:  
435 (A) LENGTH: 15 amino acids  
436 (B) TYPE: amino acid  
437 (C) STRANDEDNESS: single-stranded  
438 (D) TOPOLOGY: linear  
439  
--> 440 (ii) ~~TYPE OF MOLECULE: peptide~~  
441  
442 (iii) HYPOTHETICAL: NO  
443  
444 (iv) ANTI-SENSE: YES  
445

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:09

INPUT SET: S35457.raw

446 (v) FRAGMENT TYPE: internal fragment

447

448 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

449

450 Glu Thr Thr Asn Val Gln Gly Trp Val Cys Leu Phe Gln Ile Thr

451 1 5 10 15

452

453 (2) INFORMATION FOR SEQ ID NO: 21:

454

455 (i) SEQUENCE CHARACTERISTICS:

456 (A) LENGTH: 15 amino acids

457 (B) TYPE: amino acid

458 (C) STRANDEDNESS: single-stranded

459 (D) TOPOLOGY: linear

460

--> 461 (ii) ~~TYPE OF MOLECULE: peptide~~

462

463 (iii) HYPOTHETICAL: NO

464

465 (iv) ANTI-SENSE: YES

466

467 (v) FRAGMENT TYPE: internal fragment

468

469 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

470

471 Gln Gly Trp Val Cys Leu Phe Gln Ile Thr His Gly Lys Ala Asp

472 1 5 10 15

473

474 (2) INFORMATION FOR SEQ ID NO: 22:

475

476 (i) SEQUENCE CHARACTERISTICS:

477 (A) LENGTH: 15 amino acids

478 (B) TYPE: amino acid

479 (C) STRANDEDNESS: single-stranded

480 (D) TOPOLOGY: linear

481

--> 482 (ii) ~~TYPE OF MOLECULE: peptide~~

483

484 (iii) HYPOTHETICAL: NO

485

486 (iv) ANTI-SENSE: YES

487

488 (v) FRAGMENT TYPE: internal fragment

489

490 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

491

492 Tyr Asn Arg Asn Ala Val Pro Asn Leu Arg Gly Asp Leu Gln Val

493 1 5 10 15

494

495

496 (2) INFORMATION FOR SEQ ID NO: 23:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:10

INPUT SET: S35457.raw

497  
498 (i) SEQUENCE CHARACTERISTICS:  
499 (A) LENGTH: 15 amino acids  
500 (B) TYPE: amino acid  
501 (C) STRANDEDNESS: single-stranded  
502 (D) TOPOLOGY: linear  
503  
--> 504 (ii) ~~TYPE OF MOLECULE: peptide~~  
505  
506 (iii) HYPOTHETICAL: NO  
507  
508 (iv) ANTI-SENSE: YES  
509  
510 (v) FRAGMENT TYPE: internal fragment  
511  
512 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
513  
514 Glu Ile Lys Ala Leu Phe Leu Ser Arg Thr Thr Gly Lys Met Glu  
515 1 5 10 15  
516

---

517 (2) INFORMATION FOR SEQ ID NO: 24:  
518  
519 (i) SEQUENCE CHARACTERISTICS:  
520 (A) LENGTH: 15 amino acids  
521 (B) TYPE: amino acid  
522 (C) STRANDEDNESS: single-stranded  
523 (D) TOPOLOGY: linear  
524  
--> 525 (ii) ~~TYPE OF MOLECULE: peptide~~  
526  
527 (iii) HYPOTHETICAL: NO  
528  
529 (iv) ANTI-SENSE: YES  
530  
531 (v) FRAGMENT TYPE: internal fragment  
532  
533 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
534  
535 Cys Trp Leu Asn Ala Ile Leu Gln Leu Phe Arg Tyr Val Glu Glu  
536 1 5 10 15  
537

---

538 (2) INFORMATION FOR SEQ ID NO: 25:  
539  
540 (i) SEQUENCE CHARACTERISTICS:  
541 (A) LENGTH: 15 amino acids  
542 (B) TYPE: amino acid  
543 (C) STRANDEDNESS: single-stranded  
544 (D) TOPOLOGY: linear  
545  
--> 546 (ii) ~~TYPE OF MOLECULE: peptide~~  
547

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:10

INPUT SET: S35457.raw

548 (iii) HYPOTHETICAL: NO  
549  
550 (iv) ANTI-SENSE: YES  
551  
552 (v) FRAGMENT TYPE: internal fragment  
553  
554 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
555  
556 Arg Tyr Val Glu Glu Pro Phe Phe Asp Trp Val Tyr Ser Ser Pro  
557 1 5 10 15  
558  
559

---

560 (2) INFORMATION FOR SEQ ID NO: 26:  
561  
562 (i) SEQUENCE CHARACTERISTICS:  
563 (A) LENGTH: 15 amino acids  
564 (B) TYPE: amino acid  
565 (C) STRANDEDNESS: single-stranded  
566 (D) TOPOLOGY: linear  
567  
--> 568 ~~(ii) TYPE OF MOLECULE: peptide~~  
569  
570 (iii) HYPOTHETICAL: NO  
571  
572 (iv) ANTI-SENSE: YES  
573  
574 (v) FRAGMENT TYPE: internal fragment  
575  
576 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
577  
578 Glu Ala Ile Lys Gln Leu Glu Asp Leu Thr Gly Leu Glu Leu His  
579 1 5 10 15  
580

---

581 (2) INFORMATION FOR SEQ ID NO: 27:  
582  
583 (i) SEQUENCE CHARACTERISTICS:  
584 (A) LENGTH: 15 amino acids  
585 (B) TYPE: amino acid  
586 (C) STRANDEDNESS: single-stranded  
587 (D) TOPOLOGY: linear  
588  
--> 589 ~~(ii) TYPE OF MOLECULE: peptide~~  
590  
591 (iii) HYPOTHETICAL: NO  
592  
593 (iv) ANTI-SENSE: YES  
594  
595 (v) FRAGMENT TYPE: internal fragment  
596  
597 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
598

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:10

INPUT SET: S35457.raw

599 Asn-Ile-Lys-His-Leu-Leu-His-Thr-Gly-Ile-Gly-Thr-Ala-Ser-Arg  
600 1 5 10 15  
601

---

602 (2) INFORMATION FOR SEQ ID NO: 28:

603

604 (i) SEQUENCE CHARACTERISTICS:

605 (A) LENGTH: 15 amino acids

606 (B) TYPE: amino acid

607 (C) STRANDEDNESS: single-stranded

608 (D) TOPOLOGY: linear

609

--> 610 (ii) ~~TYPE OF MOLECULE: peptide~~

611

612 (iii) HYPOTHETICAL: NO

613

614 (iv) ANTI-SENSE: YES

615

616 (v) FRAGMENT TYPE: internal fragment

617

618 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

619

620 Ala-Ile-Asp-Asp-Glu-Asp-Phe-Tyr-Pro-Trp-Thr-Pro-Asp-Pro-Ser

621 1 5 10 15

622

623

---

624 (2) INFORMATION FOR SEQ ID NO: 29:

625

626 (i) SEQUENCE CHARACTERISTICS:

627 (A) LENGTH: 15 amino acids

628 (B) TYPE: amino acid

629 (C) STRANDEDNESS: single-stranded

630 (D) TOPOLOGY: linear

631

--> 632 (ii) ~~TYPE OF MOLECULE: peptide~~

633

634 (iii) HYPOTHETICAL: NO

635

636 (iv) ANTI-SENSE: YES

637

638 (v) FRAGMENT TYPE: internal fragment

639

640 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

641

642 Thr-Pro-Asp-Pro-Ser-Asp-Val-Leu-Val-Phe-Val-Pro-Tyr-Asp-Gln

643 1 5 10 15

644

---

645 (2) INFORMATION FOR SEQ ID NO: 30:

646

647 (i) SEQUENCE CHARACTERISTICS:

--&gt; 648 (A) LENGTH: 15 amino acids

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:11

INPUT SET: S35457.raw

649 (B) TYPE: amino acid  
650 (C) STRANDEDNESS: single-stranded  
651 (D) TOPOLOGY: linear  
652  
--> 653 (ii) ~~TYPE OF MOLECULE: peptide~~  
654  
655 (iii) HYPOTHETICAL: NO  
656  
657 (iv) ANTI-SENSE: YES  
658  
659 (v) FRAGMENT TYPE: internal fragment  
660  
661 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30  
662  
--> 663 Thr Asp Leu Gln Lys Mt Val Met Gly Asn Thr Lys Pro Val Glu  
664 1 5 10 15  
665

*Error*

*invalid amino descriptor (met)?*

---

666 (2) INFORMATION FOR SEQ ID NO: 31:  
667  
668 (i) SEQUENCE CHARACTERISTICS:  
669 (A) LENGTH: 15 amino acids  
670 (B) TYPE: amino acid  
671 (C) STRANDEDNESS: single-stranded  
672 (D) TOPOLOGY: linear  
673  
--> 674 (ii) ~~TYPE OF MOLECULE: peptide~~  
675  
676 (iii) HYPOTHETICAL: NO  
677  
678 (iv) ANTI-SENSE: YES  
679  
680 (v) FRAGMENT TYPE: internal fragment  
681  
682 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
683  
684 Met Leu Ser Asp Ala Ala Leu Met Val Leu His Arg Gly Asn Arg  
685 1 5 10 15  
686  
687

---

688 (2) INFORMATION FOR SEQ ID NO: 32:  
689  
690 (i) SEQUENCE CHARACTERISTICS:  
691 (A) LENGTH: 15 amino acids  
692 (B) TYPE: amino acid  
693 (C) STRANDEDNESS: single-stranded  
694 (D) TOPOLOGY: linear  
695  
--> 696 (ii) ~~TYPE OF MOLECULE: peptide~~  
697  
698 (iii) HYPOTHETICAL: NO  
699



RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:11

INPUT SET: S35457.raw

700 (iv) ANTI-SENSE: YES  
701  
702 (v) FRAGMENT TYPE: internal fragment  
703  
704 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
705  
706 Leu-Leu Lys Met Lys Ala His Ile Asp Pro Glu Pro His His Glu  
707 1 5 10 15  
708

---

709 (2) INFORMATION FOR SEQ ID NO: 33:  
710  
711 (i) SEQUENCE CHARACTERISTICS:  
712 (A) LENGTH: 15 amino acids  
713 (B) TYPE: amino acid  
714 (C) STRANDEDNESS: single-stranded  
715 (D) TOPOLOGY: linear  
716  
--> 717 ~~(ii) TYPE OF MOLECULE: peptide~~  
718  
719 (iii) HYPOTHETICAL: NO  
720  
721 (iv) ANTI-SENSE: YES  
722  
723 (v) FRAGMENT TYPE: internal fragment  
724  
725 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
726  
727 Pro Phe Phe Phe Ser Asp Val Arg Ser Asn Phe Ser Lys Leu Val  
728 1 5 10 15  
729

---

730 (2) INFORMATION FOR SEQ ID NO: 34:  
731  
732 (i) SEQUENCE CHARACTERISTICS:  
733 (A) LENGTH: 14 amino acids  
734 (B) TYPE: amino acid  
735 (C) STRANDEDNESS: single-stranded  
736 (D) TOPOLOGY: linear  
737  
--> 738 ~~(ii) TYPE OF MOLECULE: peptide~~  
739  
740 (iii) HYPOTHETICAL: NO  
741  
742 (iv) ANTI-SENSE: YES  
743  
744 (v) FRAGMENT TYPE: internal fragment  
745  
746 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
747  
748 Ala Pro Val Leu Leu Ala Gly Leu Val Lys Val Ala Ser Ser  
749 1 5 10  
750

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:11

INPUT SET: S35457.raw

751

---

752 (2) INFORMATION FOR SEQ ID NO: 35:

753

754 (i) SEQUENCE CHARACTERISTICS:

755 (A) LENGTH: 14 amino acids

756 (B) TYPE: amino acid

757 (C) STRANDEDNESS: single-stranded

758 (D) TOPOLOGY: linear

759

--> 760 (ii) ~~TYPE OF MOLECULE: peptide~~

761

762 (iii) HYPOTHETICAL: NO

763

764 (iv) ANTI-SENSE: YES

765

766 (v) FRAGMENT TYPE: internal fragment

767

768 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

769

770 Ala Gly Leu Val Lys Val Ala Ser Ser Phe Phe Arg Ser Thr

771 1 5 10

772

---

773 (2) INFORMATION FOR SEQ ID NO: 36:

774

775 (i) SEQUENCE CHARACTERISTICS:

776 (A) LENGTH: 14 amino acids

777 (B) TYPE: amino acid

778 (C) STRANDEDNESS: single-stranded

779 (D) TOPOLOGY: linear

780

--> 781 (ii) ~~TYPE OF MOLECULE: peptide~~

782

783 (iii) HYPOTHETICAL: NO

784

785 (iv) ANTI-SENSE: YES

786

787 (v) FRAGMENT TYPE: internal fragment

788

789 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

790

791 Val Ala Ser Ser Phe Phe Arg Ser Thr Pro Glu Asp Leu Glu

792 1 5 10

793

---

794 (2) INFORMATION FOR SEQ ID NO: 37:

795

796 (i) SEQUENCE CHARACTERISTICS:

797 (A) LENGTH: 14 amino acids

798 (B) TYPE: amino acid

799 (C) STRANDEDNESS: single-stranded

800 (D) TOPOLOGY: linear

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:12

INPUT SET: S35457.raw

801  
--> 802 (ii) ~~TYPE OF MOLECULE: peptide~~  
803  
804 (iii) HYPOTHETICAL: NO  
805  
806 (iv) ANTI-SENSE: YES  
807  
808 (v) FRAGMENT TYPE: internal fragment  
809  
810 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
811  
812 Phe Phe Arg Ser Thr Pro Glu Asp Leu Glu Arg Ala Glu Lys  
813 1 5 10  
814  
815

---

816 (2) INFORMATION FOR SEQ ID NO: 38:  
817  
818 (i) SEQUENCE CHARACTERISTICS:  
819 (A) LENGTH: 14 amino acids  
820 (B) TYPE: amino acid  
821 (C) STRANDEDNESS: single-stranded  
822 (D) TOPOLOGY: linear  
823  
--> 824 (ii) ~~TYPE OF MOLECULE: peptide~~  
825  
826 (iii) HYPOTHETICAL: NO  
827  
828 (iv) ANTI-SENSE: YES  
829  
830 (v) FRAGMENT TYPE: internal fragment  
831  
832 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
833  
834 Ile Ser Ile Pro Ser Gln Lys Ser Val Leu Tyr Phe Leu Ile  
835 1 5 10  
836

---

837 (2) INFORMATION FOR SEQ ID NO: 39:  
838  
839 (i) SEQUENCE CHARACTERISTICS:  
840 (A) LENGTH: 14 amino acids  
841 (B) TYPE: amino acid  
842 (C) STRANDEDNESS: single-stranded  
843 (D) TOPOLOGY: linear  
844  
--> 845 (ii) ~~TYPE OF MOLECULE: peptide~~  
846  
847 (iii) HYPOTHETICAL: NO  
848  
849 (iv) ANTI-SENSE: YES  
850  
851 (v) FRAGMENT TYPE: internal fragment

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:12

INPUT SET: S35457.raw

852  
853 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
854  
855 Lys Arg Gln Lys Met Val Asp Asp Ala Val Asn Glu Tyr Ile  
856 1 5 10  
857

---

858 (2) INFORMATION FOR SEQ ID NO: 40:  
859  
860 (i) SEQUENCE CHARACTERISTICS:  
861 (A) LENGTH: 14 amino acids  
862 (B) TYPE: amino acid  
863 (C) STRANDEDNESS: single-stranded  
864 (D) TOPOLOGY: linear  
865  
--> 866 ~~(ii) TYPE OF MOLECULE: peptide~~  
867  
868 (iii) HYPOTHETICAL: NO  
869  
870 (iv) ANTI-SENSE: YES  
871  
872 (v) FRAGMENT TYPE: internal fragment  
873  
874 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
875  
876 Asn Glu Tyr Ile Glu Lys Ala Asn Ile Thr Thr Asp Asp Lys  
877 1 5 10  
878  
879

---

880 (2) INFORMATION FOR SEQ ID NO: 41:  
881  
882 (i) SEQUENCE CHARACTERISTICS:  
883 (A) LENGTH: 14 amino acids  
884 (B) TYPE: amino acid  
885 (C) STRANDEDNESS: single-stranded  
886 (D) TOPOLOGY: linear  
887  
--> 888 ~~(ii) TYPE OF MOLECULE: peptide~~  
889  
890 (iii) HYPOTHETICAL: NO  
891  
892 (iv) ANTI-SENSE: YES  
893  
894 (v) FRAGMENT TYPE: internal fragment  
895  
896 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
897  
898 Thr Asp Asp Lys Thr Leu Asp Glu Ala Glu Lys Ser Pro Leu  
899 1 5 10  
900

---

901 (2) INFORMATION FOR SEQ ID NO: 42:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:12

INPUT SET: S35457.raw

902  
903 (i) SEQUENCE CHARACTERISTICS:  
904 (A) LENGTH: 14 amino acids  
905 (B) TYPE: amino acid  
906 (C) STRANDEDNESS: single-stranded  
907 (D) TOPOLOGY: linear  
908  
--> 909 (ii) ~~TYPE OF MOLECULE: peptide~~  
910  
911 (iii) HYPOTHETICAL: NO  
912  
913 (iv) ANTI-SENSE: YES  
914  
915 (v) FRAGMENT TYPE: internal fragment  
916  
917 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
918  
919 Thr Val Gly Phe Arg Glu Arg Thr Leu Pro Gly Gln Lys Ala  
920 1 5 10  
921

---

922 (2) INFORMATION FOR SEQ ID NO: 43:  
923  
924 (i) SEQUENCE CHARACTERISTICS:  
925 (A) LENGTH: 14 amino acids  
926 (B) TYPE: amino acid  
927 (C) STRANDEDNESS: single-stranded  
928 (D) TOPOLOGY: linear  
929  
--> 930 (ii) ~~TYPE OF MOLECULE: peptide~~  
931  
932 (iii) HYPOTHETICAL: NO  
933  
934 (iv) ANTI-SENSE: YES  
935  
936 (v) FRAGMENT TYPE: internal fragment  
937  
938 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
939  
940 Asp Asp Val Asn Ser Glu Pro Ala Gln Pro Val Glu Glu Gln  
941 1 5 10  
942  
943

---

944 (2) INFORMATION FOR SEQ ID NO: 44:  
945  
946 (i) SEQUENCE CHARACTERISTICS:  
947 (A) LENGTH: 14 amino acids  
948 (B) TYPE: amino acid  
949 (C) STRANDEDNESS: single-stranded  
950 (D) TOPOLOGY: linear  
951  
--> 952 (ii) ~~TYPE OF MOLECULE: peptide~~

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:13

INPUT SET: S35457.raw

953  
954 (iii) HYPOTHETICAL: NO  
955  
956 (iv) ANTI-SENSE: YES  
957  
958 (v) FRAGMENT TYPE: internal fragment  
959  
960 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
961  
962 Asn Thr Gly Ser Ile Ile Asn Asn Tyr Tyr Met Gln Gln Tyr  
963 1 5 10  
964

---

965 (2) INFORMATION FOR SEQ ID NO: 45:

966  
967 (i) SEQUENCE CHARACTERISTICS:  
968 (A) LENGTH: 14 amino acids  
969 (B) TYPE: amino acid  
970 (C) STRANDEDNESS: single-stranded  
971 (D) TOPOLOGY: linear

--> 972  
973 (ii) ~~TYPE OF MOLECULE: peptide~~

974  
975 (iii) HYPOTHETICAL: NO  
976  
977 (iv) ANTI-SENSE: YES  
978  
979 (v) FRAGMENT TYPE: internal fragment  
980

981 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

982  
983 Gly Pro Tyr Ala Gly Pro Leu Glu Arg Gln Lys Pro Leu Lys  
984 1 5 10  
985

---

986 (2) INFORMATION FOR SEQ ID NO: 46:

987  
988 (i) SEQUENCE CHARACTERISTICS:  
989 (A) LENGTH: 14 amino acids  
990 (B) TYPE: amino acid  
991 (C) STRANDEDNESS: single-stranded  
992 (D) TOPOLOGY: linear

--> 993  
994 (ii) ~~TYPE OF MOLECULE: peptide~~

995  
996 (iii) HYPOTHETICAL: NO  
997  
998 (iv) ANTI-SENSE: YES  
999  
1000 (v) FRAGMENT TYPE: internal fragment  
1001

1002 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

1003

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:13

INPUT SET: S35457.raw

1004 Pro Leu Glu Arg Gln Lys Pro Leu Lys Val Arg Ala Lys Leu  
1005 1 5 10  
1006  
1007

---

1008 (2) INFORMATION FOR SEQ ID NO: 47:

1009

1010 (i) SEQUENCE CHARACTERISTICS:

1011 (A) LENGTH: 14 amino acids

1012 (B) TYPE: amino acid

1013 (C) STRANDEDNESS: single-stranded

1014 (D) TOPOLOGY: linear

1015

--> 1016 (ii) ~~TYPE OF MOLECULE: peptide~~

1017

1018 (iii) HYPOTHETICAL: NO

1019

1020 (iv) ANTI-SENSE: YES

1021

1022 (v) FRAGMENT TYPE: internal fragment

1023

1024 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

1025

1026 Gly Pro Tyr Ala Gly Pro Met Glu Arg Gln Lys Pro Leu Lys

1027 1

1028

1029 (2) INFORMATION FOR SEQ ID NO: 48:

1030

1031 (i) SEQUENCE CHARACTERISTICS:

1032 (A) LENGTH: 14 amino acids

1033 (B) TYPE: amino acid

1034 (C) STRANDEDNESS: single-stranded

1035 (D) TOPOLOGY: linear

1036

--> 1037 (ii) ~~TYPE OF MOLECULE: peptide~~

1038

1039 (iii) HYPOTHETICAL: NO

1040

1041 (iv) ANTI-SENSE: YES

1042

1043 (v) FRAGMENT TYPE: internal fragment

1044

1045 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

1046

1047 Pro Met Glu Arg Gln Lys Pro Leu Lys Val Lys Ala Lys Ala

1048 1 5 10 10

1049

1050

# SEQUENCE VERIFICATION REPORT

## PATENT APPLICATION US/09/254,966

DATE: 01/25/2001  
TIME: 23:33:13

INPUT SET: S35457.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i)APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Bayer Aktiengesellschaft
27	Unknown or Misplaced Identifier	(A) CURRENT APPLICATION NUMBER:09/254,966
28	Unknown or Misplaced Identifier	(B) CURRENT APPLICATION FILING DATE: March 16
29	Unknown or Misplaced Identifier	(C) PRIOR APPLICATION NUMBER:PCT/EP97/04866
30	Unknown or Misplaced Identifier	(D) PRIOR APPLICATION FILING DATE:September 8, 1
40	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
61	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
82	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
103	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
124	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
145	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
166	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
187	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
208	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
229	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
250	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
271	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
292	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
313	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
334	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
355	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
376	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
397	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
418	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
440	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
461	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
482	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
504	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
525	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
546	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
568	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
589	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
610	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
632	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
648	Entered (15) and Calc. Seq. Length (14) differ	(A) LENGTH: 15 amino acids
653	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
663	Wrong Amino Acid Designator	Thr Asp Leu Gln Lys Mt Val Met Gly Asn Thr Lys Pro Val
674	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
696	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
717	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
738	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
760	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
781	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
802	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
824	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
845	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
866	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide



**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/254,966**DATE: 01/25/2001  
TIME: 23:33:14**INPUT SET: S35457.raw**

Line	Error	Original Text
888	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
909	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
930	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
952	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
973	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
994	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
1016	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide
1037	Unknown or Misplaced Identifier	(ii)TYPE OF MOLECULE: peptide

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/09/254,966DATE: 01/25/2001  
TIME: 23:33:14

INPUT SET: S35457.raw

Line	Original Text	Corrected Text
17	(E) ZIP CODE:15205-9741	(E) ZIP:15205-9741
20	(v)COMPUTER-READABLE FORM:	(v) COMPUTER READABLE FORM:
44	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
65	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
86	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
107	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
128	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
149	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
170	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
191	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
212	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
233	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
254	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
275	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
296	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
317	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
338	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
359	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
380	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
401	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
422	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
444	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
465	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
486	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
508	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
529	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
550	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
572	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
593	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
614	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
636	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
657	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
678	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
700	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
721	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
742	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
764	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
785	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
806	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
828	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
849	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
870	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
892	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
913	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
934	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
956	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
977	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
998	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES

PAGE: 2

**SEQUENCE CORRECTION REPORT**  
**PATENT APPLICATION US/09/254,966**

DATE: 01/25/2001  
TIME: 23:33:14

*INPUT SET: S35457.raw*

Line	Original Text	Corrected Text
1020	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES
1041	(iv)ANTISENSE: YES	(iv) ANTI-SENSE: YES